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Charles Control

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http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics (2001)
Contact: BayGenomics (2001)
Contact: BayGenomics (2001)
Contact: BayGenomics (2001)
Bay Area Functional Genomics Consortium (BayGenomics)
Bmail: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
information available from
CELL_LINEKEY=RS1325
CELL_LINEKEY=RS1325
CIBL_LINEKEY=RS1325
CIBSE: Gene Trap.
Location/Qualifiers
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409) Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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RST325 BayGenomics Gene Trap Library pGT2TMpfa Mus musculus cDNA,
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Best Local Similarity 79.2%; Pred. No. 1.3e+05;
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Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGLYBY73 30 bp DNA linear GSS 06-MAR-2004 Pan troglodytes DNA, clone: RP43-079M17.T7, genomic survey sequence.
                                                      AA878803 25 bp mRNA linear EST 14-APR-1998 of86e04.sl NCI CGAP Li5 Homo sapiens CDNA clone IMAGE:1437246 3' similar to SW:FRPM HUMAN P10161 SALIVARY PROLINE-RICH FROTEIN PO contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Lis"
/note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 0.8 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                          Hominidae, Homo.
1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43
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Pred. No. 1.3e+05;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Trace considered overall poor quality
Insert Length: 185 Std Error: 0.00
Seq primer: -40mil Wd. Er from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1437246"
/tissue_type="hepatic adenoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 CCGCTGGGGACTTTCCAGGGGGAC 33
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                                                                                                                                                                          AA878803.1 GI:2987768
                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                               Homo sapiens
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Best Local Similarity
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                  RESULT 2
AA878803/c
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AG198773/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 716
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; Contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 716 Std Brror: 0.00
Seq primer: MIJRP;
High quality sequence stop: 1.
High quality sequence stop: 1.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Indels
 5
0; Mismatches
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/mol_type="mRNA"
/db_xref="GDB:572930"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:158876"
sex="Female"
                            4 GACTITCCGCTGGGGACTITCCAG 27
                                                   26 GACTTTCCGCTGGGGTGTCACCCG 3
                                                                                                                                                                                                                                                                                                                                                                        Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                             R75772.1 GI:850454
19; Conservative
                                                                                                                                                                                 R75772
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Matches
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4;

41.1%; Score 15.6; DB 8; llarity 81.8%; Pred. No. 1.9e+05; Conservative 0; Mismatches 4;

Query Match Best Local Similarity Matches 18; Conserv

Length 37; Indels

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/done lib="Gm-clool"
/note="Wettor: pBluescript II XR; Site 1: ECORI; Site 2:
Xhoi; Immature Cotyledon CDNA. The mRNA was isolated and
then Stratagene's CDNA Synthesis Kit (catalog #2010401) was
used to synthesize the CDNA. First-strand synthesis was
performed with 5-methyl dCTP, hence the ligated CDNA is
hemimethylated. Stratagene's first-strand synthesis primer
was used (GAGAGAGAGAGAGACACACACTGTCTGAG(T)-18]. After
second-strand synthesis, the CDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the CDNA would be protected by their
hemimethylated status. The CDNA constructs were
size-fractionated with a 500bp cutoff, using GibcoBRL Life
Technologie s' CDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+) that had been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khamn, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Public Soybean EST Project
Umpublished (1999)
Other ESTS: salobot, Yublic Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                  A1416657 23-JUL-2004 sal0b04.xl Gm-c1003 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1003-8 3' similar to WP:W03D2.1 CE14506 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons; rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watcon.wustl.edu
When it has been determined, an EST from the other end of this
When it has been determined, an clone' field. Other ESTs:
salobe4.yl GENOWE SYSTEMS CLONE ID: Gm-cl003-8 Trace considered
overall poor quality Possible reversed clone: similarity on wrong
strand This clone is available through: Biogenetic Services, 801
32nd Ave. Brookings, 20 57006 USA (phone: 800 423 4163; email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/dl_one="GENOME SYSTEMS CLONE ID: G

/tissue_type="immature cotyledon"

/lab_hoste="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Glycine max"
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/cultivar="Williams"
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6 CTTTCCGCTGGGGACTTTCCAG 27
                                                         24
                                       CTTTCCGCTGGCCCTCTTCAG
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AI416657
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Franch Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Guzchontoglires; Glires; Rodentia; Ciorognathi; Muroidea; Muridae; Murinae; Mus.

1 (Dassa 1 to 34)

1 (Danses 1 to 34)

1 (Dan, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmod, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ760788 16-FEB-200 1MO554F14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0554F14 R, genomic survey sequence.
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/close_lib="Mouse=10kb plasmid UGCOM library"
/note="Wector: PWD4Zlv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                   Length 34;
                                                                                                                                                               Indels
         Bento Soares and M. Fatima Bonaldo.
                                                                                            Query Match
40.5%; Score 15.4; DB 1;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 22; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: F column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
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                                                                                                                                                                                                                              6 CTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0554F14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ760788.1 GI:12869009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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AZ760788
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| Organism="Homo sapiens"
| wol_type="mRNM"
| db_xref="texon:9606"
| dlone="IMAGB:2006006"
| fissue_type="pooled germ cell tumors"
| tab host="pooled germ cell tumors"
| lab host="pooled germ cell tumors"
| lab host="bollom"
| lone="locitic": pT713D=pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco sligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI altes of the modified pT7T3 vector. Library is normalized. Library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene index.
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n=15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Plagsteaff, Az 86011, Phone: 520-523-1078 (Dr. Paul Keim) 520-523-1078 (Dr. 520-523-7500 email: paul.keim@ana.edu
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A1357237

A14 bp mRNA linear EST 15-FEB-1999 qx63308.x1 NCI CGAP GC4 HOMO sapient cDNA clone IMAGE:2006006 3' similar to SW:PRP2 HUWAN PO2812 SALIVARY PROLINE-RICH PROTEIN PRECURSOR ;contains element MSR1 repetitive element ;, mRNA
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1 (Dases 1 to 34)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.5%; Score 15.4; DB 1; Length 28; Best Local Similarity 76.0%; Pred. No. 2.2e+05; Matches 19; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                       University of Illinois"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TTTCCGCTGGGGACTTTCCAGGGGG 31
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Homo sapiens
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Class: transposon-tagged
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GSS.
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AI917121.1 GI:5636976
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                                                                                                                                                survey sequence.
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Zea mays
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AUTHORS
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JOURNAL
COMMENT
                                 RESULT 10
CG776618
LOCUS
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/mol type="ganomic DNA"
/mol type="aganomic DNA"
/do_xref="last"
/dev_stage="last"
/dev_stage="l
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1 (bases 1 to 50)
Walbot, V.
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Unpublished (2001)
Contact: Walbot V
chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanford University
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2227
Email: walbot@stanford.edu
Email: walbot@stanford.edu
Reverse complemented post-ligation sequence from source sequence.
Plate: 1118010 row: 20
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                                                                                                                         Query Match 40.5%; Score 15.4; DB 9; Length 34; Best Local Similarity 76.0%; Pred. No. 2.2e+05; Matches 19; Conservative 0; Mismatches 6; Indels
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GG80.335.1 GI:38236121
GSS.
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Zea mays
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CG800335/c
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/ Adv gatge="adult"
/ RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.ramb.iastate-edu' and follow the links for
'RescueMu.' Grid L was grown in Molokai in 2001. DNA was
extracted from leaf strips, double digested using BamHI
and Bgill, and ligated to form circular plasmids. DH10B
ampicillin."
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ts52a12.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:2232190 3' similar to SW:CA13 EOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN.
contains element TAR1 repetitive element; , mRNA sequence.
CG776618 42 bp DNA linear GSS 29-OCT-2003
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Unpublished (2001)
Contact: Walbot V
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1123002 row: 2
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/cultivar="mixed background W23/A188/B73/K55"
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Stanford University
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SOURCE
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ころ ナランス

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CL878011 38 bp DNA linear GSS 30-AUG-2004 abf23b12.x1 Soybean random, unfiltered genomic library Glycine max
Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 28-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU106243 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AUSE00166, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                         /clone_ib="CAS09420"
/clone_lib="Sugano Homo sapiens cDNA library"
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/clone_lib="Sugano Homo sapiens cDNA library"
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Institute of Medical Science, University of Tokyo
44-6-1, Elizokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                         Length 50;
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                                                                                                                                                                                                                                                                                         Score 14.6; DB 1;
Pred. No. 4.7e+05;
0; Mismatches 9;
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                                                                                               1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                              1997).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                           38.4%;
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                                                                                                                                                                                                                                                                                                                                           20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149-156 (1997)
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AU106243/c
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KEYWORDS
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:2232190"
/tissue_type="renal cell tumor"
/lab host="nBiloB"
/clone_lib="NCI CGAP_Kid8"
/clone_lib="NCI CGAP_Kid8"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_l: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.2 kb. Life Technologies catalog #:
11524-014"
                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E, Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
     Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
                                               Hominidae; Homo.

1 (bases 1 to 46)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal Minatoku, Tokyo 108-8639, Japan
Emali: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                 ww-bio.llnI.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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EMBO Rep. 2 (5), 388-393 (2001)
11375929
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                                                                                                                                               Tumor Gene Index
Unpublished (1997)
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Matches 20; Conserv
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A2345648 10kb plasmid UUGCIM library Mus musculus genomic Clone UUGCIM0080K22 F, genomic survey sequence.
                                                                                                                                                                                   /moltope="genomic DNA"
/moltope="genomic DNA"
/moltope="genomic DNA"
/deotype="col-0"
/db_xref="taxon:3702"
/clone="SALK G22130.29.10.x"
/clone="SALK G22130.29.10.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PGCK was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
flirectly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                        This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At5917610.
Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.9%; Score 14.4; DB 9; 75.0%; Pred. No. 5.5e+05; tive 0; Mismatches 6;

    42
/organism="Arabidopsis thaliana"

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Insert Length: 10000 Std Error: 0.00
Plate: 0080 Tow: K column: 22
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/drain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0080K22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 45.
Location/Qualifiers
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                                                                                                                            Location/Qualifiers
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    Fax: 858 558 6379
Email: ecker@salk.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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AUTHORS
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AZ345648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Glycine max"
/mol type="genomic DNA"
/cultivar="Williams 82"
/db.xref="taxon:3847"
/tione_lib="Soybean random, unfiltered genomic library"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstX1; Randomly sheared
genomic DNA ranging from 0.7-1.5 kb were end repaired and
ligated to BstX1 linkers prior to cloning in BstX1-cut
pOT2. LibID: 230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                1 (bases 1 to 38)
Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                  Methylation filtered genomic sequences from Glycine max Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
1010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Score 14.4; DB 10;
llarity 93.8%; Pred. No. 5.4e+05;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                             Contact: Gary Stacey
University of Missouri
University of Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smail: staceyg@missouri.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burvey sequence.
BZ288740
BZ288740.1 GI:24329178
                    CL878011
CL878011.1 GI:51610429
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                                                                                   Glycine max (soybean)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: shotgun.
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nes 15; Conserv
                                                                                                                                                                                                                                                                                    Stacey, G.
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and caracterization of a full
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 28-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 bp mRNA linear EST 28-JAN-200
AU106577 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT03453, mRNA sequence.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases Homo.

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Sazuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Sakuki,Y., Nakamura,Y., Tangai,T., Yangara,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
mapping of mRNA start sites
mapping of Sp. 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 5.6e+05;
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/db_xref="taxon:9606"
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                                                                                                              (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql 47321141gbl AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
I Chaese I to 40.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
muscula C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aa59c05.rl NCI CGAP GCB1 Homo Sapiens CDNA linear EST 18-AUG-1: similar to SW:YET7 YEAST P40066 HYPOTHETICAL 40.5 KD PROTEIN IN NUP157-SW14 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.9%; Score 14.4; DB 9; Length 45; ilarity 75.0%; Pred. No. 5.6e+05; Conservative 0; Mismatches 6; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:82524"
/tissue_type="germinal center B cell"
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Unpublished (1997)
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Matches 18; Conserv
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GSS 07-APR-2005
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Lewinski, M.K., Bisgrove, D., Shinn, P., Chen, H., Hoffmann, C.,
Hannenhalli, S., Verdin, B., Berry, C.C., Ecker, J.R. and Bushman, F.D.
Genome-wide analysis of chromosomal features repressing human
immunodeficiency virus transcription
J. Virol. 79 (11), 6610-6619 (2005)
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                           CZ442924

1BB3GO2.fwd HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells Homo sapiens genomic clone IBB3G02.fwd, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription and suggest models for transcriptional
latency in cells from HIV-infected patients."
                                                                                                                                                                                                                                                                                                                 Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA
19104-6076, USA
                                                                                                                                                                                                                                                                                                                                                                              Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                            Class: PCR with specific primers.
Location/Qualifiers
                                                                                                 CZ442924.1 GI:62379025
                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                           Contact: Bushman FD
                                                                                                                                               Homo sapiens
                         LOCUS
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KEYWORDS
SOURCE
ORGANISM
RESULT 19
CZ442924/c
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Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 bp mRNA linear EST 28-AUG-1998 ox33b01.81 Soares total fetus ND2HF8 9w Homo sapiens cDNA clone IMAGE:1658089 3' Similar to SW:PP11_PIG P51524 PROPHENIN-1 AI039253
                                                                                                                                                GSS 13-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrell, Oxford University rives, Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                         37 bp DNA linear GSS 13-DE
T. brucei sheared genomic DNA clone 379b06, reverse sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                      Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 6.4e+05,
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/strain="TREU927"
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                           27 GGTGAGTACTCTGCAGGAGGACGTTAC 1
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/clone="379b06"
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Trypanosoma brucei
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(bases 1 to 37)
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Gaps

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Score 14.2; DB 10; Length 35; Pred. No. 6.4e+05; 0; Mismatches 8; Indels (

Query Match 37.4%; Best Local Similarity 70.4%; Matches 19; Conservative (

Short St. Act.

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CC459460 50 bp DNA linear GSS 30-MAY-2003 SALK 129954.28.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_129954.28.55.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
dadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:3702"
/clone="SALK 129954.28.55.x"
/clone="SALK 129954.28.55.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                              /clone="ADSE00350"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                               Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                             Score 14.2; DB 1;
Pred. No. 6.7e+05;
0; Mismatches 8;
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/mol_type="genomic DNA"
/ecotype="Col-0"
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Pred. No. 6.7e+05;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
  organism="Homo sapiens"
                                                                                                                                                                                                                                     1 GGGGACTITCCGCTGGGGACTITCCAG 27
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                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADSE00350"
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                                                                                                                                               Query Match
Best Local Similarity 70.4%;
Matches 19; Conservative
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Unpublished (2001)
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                        Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bemail: ysuzuki@ima.u-ckyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1199-156 (1997).
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AU104208 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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I Chases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ote, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1067 Std Brror: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Bento Soares and M. Fatima Bonaldo. "
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/organism="Homo sapiens"
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AU104208
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Homo sapiens
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/clone='IMAGE:1571809"
/tissue_type="pooled germ cell tumors"
/tissue_type="pooled germ cell tumors"
/lab_hote="blublubs"
/clone lib="NCI CGAP GC4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Tector: pT7T3D-Pac (Pharmacia) with a modified
polylimer; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Bco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Bco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
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Pan troglodytes DNA, clone: RP43-065002.TJ, genomic survey
sequence.
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                                                                                                                                                                                                                                                                   Sequencing Center
information can be
                                                                                                                          Email: cgapbs.romail.infl.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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    .34
    /organism="Homo sapiens"
/mol_type="mRNA"
    /db_xref="taxon:9606"

                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Pan troglodytes
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AG190424.1 GI:45222600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-50T-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (Rittp://www.genoplante.com and http://genoplante-info.infopiogen.fr).

Location/Qualifiers
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                         AJ587887 50 bp DNA linear GSS 15-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                           Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F., Chauvin, S., Bechlold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                    Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                        336H01, genomic survey sequence.
AJ587887.1 GI:37937511
GSS, left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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left border"
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EMBO Rep. 3 (12), 1152-1157 (2002)
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1 (bases 1 to 34)
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AA931137/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb12 (gilfa732114 [gb] AF125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 40)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)
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1M0545P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0545P18 F, genomic survey sequence.
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 36.8%; Score 14; DB 9; Length 40; I Similarity 66.7%; Pred. No. 7.8e+05; 20; Conservative 0; Mismatches 10; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0545 row: P column: 18
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGCIM0545P18"
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Mus musculus
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Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance PALIONE tracking errors.
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Bukaryotanus

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Rolly, M., Rose, M., Rose, R., Ztokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Muse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="B. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.8%; Score 14; DB 10; Length 38; Best Local Similarity 66.7%; Pred. No. 7.7e+05; Matches 20; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddurn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0408 row: O column: 08
Seq primer: CACAAGABAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
                                                                                                                                                                                                                                                                      1. .38
/organism="Pan troglodytes"
/mol_type="genomic DNA"
db_xref="taxon:9598"
/clone="RP43-065002.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGACTITCCGCTGGGGACTTTCCAGGGGGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GGAATATTTGGGGGGAATATTCTAGGGGGA 37
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0408008"
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                         : pBACe3.6
: EcoRI
: EcoRI.
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                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                            Sequencing: TJ
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R.Site 2
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AZ595836
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GSS 14-DEC-2000

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TITLE
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                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 [gb] API29072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
//note="Wetcor: PWD42rv; Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L248/957
f05395-3prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic Sequence recovered from 3' end of piggyBac,
genomic survey sequence.
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Sequence orientation is forward strand relative to 5' end of piggyBac element.
The piggyBac element.
The piggyBac insertion position is 1 in the 40 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
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CZ487957.1 GI:62985395
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14981521
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CZ487957
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ð a source

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/close_lib="Exelixis piggyBac WH insertions"
/close_lib="Exelixis piggyBac WH (GenBank accession number AY515148); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements We remobilizate the WH element using the constitutive alpha-1 tubulin.piggyBac transposase source. We remobilized the WH element from a single ammunition element on the Binainscy balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Bmail: infoobaygenomics.ucsf.edu
Sequence tag generated by S. RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
CELL_LINE&KEY=XG205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC200179 41 bp mRNA linear GSS 09-MAY-2003
XG205 BayGenomics Gene Trap Library pGT1Lxf Mus musculus CDNA, mRNA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
1 (bases 1 to 41)
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/clone lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
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Pred. No. 7.8e+05;
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Pred. No. 7.8e+05;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
organism="Drosophila melanogaster"
                    /mol_type="genomic DNA"
/strain="isogenic w- strain"
/db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.8%; Scor.
66.7%; Pred. No. /...
0; Mismatches
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/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: Gene Trap.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://baygenomics.ucsf.edu/
Unpublished (2001)
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Mus musculus
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CC200179.1 GI:30479942
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CC200179/c
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/clone="INGGE:1466028"
/lab_host="DH10B"
/clone="Cosares"
/cosares for cosares
/cosares
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IMAGE:2011857 3'
PROTEIN 1
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(bases 1 to 49)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gen Index.

(Dipublished (1998)
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 790 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 36.8%; Score 14; DB 1; I
Similarity 77.3%; Pred. No. 7.9e+05;
17; Conservative 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                   1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UJCEO gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=G705G08' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html'
I' Inhouse Sequence Identifier: 20122
                                                                                                                                45 bp mRNA linear GSS 22-MAR-2005
G076G08 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
CL640557
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Sukarychai, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Mar 22, 2005 this sequence version replaced gi:49489004.
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
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German Genetrap Consortium (GGTC)
Email: info@genetrap.de
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/clone="G076G08"
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             26 GATATTCCTCTTGGGTCTTTCC 5
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Mus musculus
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AI432930.1 GI:4285621
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: egapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM7650 row: e column: 19

High quality sequence stop: 50.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 36.8%; Score 14; DB 1; Length 49; Similarity 60.5%; Pred. No. 8e+05; 23; Conservative 0; Mismatches 15; Indels
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                                                                         Trace considered overall poor quality Insert Length: 672 Std Error: 0.00 Seg primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                           1. .49
/organism="Homo sapiens"
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/clone="IMAGE:3158010"
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/strain="FVB/N"
/db_xref="taxon:)
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BE311372
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A. P. L. STANFAR

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Hominidae, Homo.

1 (bases 1 to 28)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015

DNA Sequencing DNA Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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28 bp mRNA linear EST 13-APR-1999 th44611.x1 NCI CGAP Lyml2 Homo sapiens CDNA clone IMAGES.2121140 3' similar to SW:PRP2 HUMAN PO2812 SALIVARY PROLINE-RICH PROTEIN PRECURSOR; contains element MSR1 repetitive element;; mRNA
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/Bex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stge="5" months"
/lab_host="DHIDB"
/lab_host="DHIDB"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammarry; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI, Cloned unidirectionally. Primer: Ōligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
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/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: Not!, Cloned unidirectionally. Primer:
Oligo dT. Areage insert size 1.25 kb. Life Technologies catalog #: 11547-015"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 8.8e+05;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                        Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                     36.8%; Score 14; DB 2; 77.3%; Pred. No. 8e+05; rative 0; Mismatches
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Insert Length: 482 Std Brror: 0.00
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 482 Std Error:
Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCGCTGGGGACTTTCCAGGG 29
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AZ628058

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/mol type="manual saplens"
/mol type="manual"
/mol type="manual"
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/doc="lynAd8:2211728"
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adenocarcinom, 7 pooled tumors"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
                                                                                                                                                                   AI579983

tq45a05.x1 NCI CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211728 3'
similar to TR:Q08805 Q08805 SALIVARY PROLINE-RICH PROTEIN L
jcontains element MSR1 repetitive element j, mRNA sequence.
AI579983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Ph.D., Dh.D., Ph.D., Ph.D., CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the L.M.G.E., Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS 22-NOV-2002
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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Danio rerio genomic clone DKEY-48J2, genomic survey sequence.
AL982948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality Insert Length: 2882 Std Brror: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1 POLYRANO.
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1 (bases 1 to 37)
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Best Local Similarity
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DR48J2S/c
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                                                                                                                                                                      GSS 13-DEC-2000
                                                                                                                                                                   AZ628058 33 bp DNA linear GSS 13-DEC-200
1M0476122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0476122 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 33)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert_Length: 10000 Std Error: 0.00
Plate: 0476 row: I column: 22
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0476122"
GGGGAATTTCCCCCGGGGCCCCCC 25
                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                               AZ628058.1 GI:11750248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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AUTHORS
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FEATURES

TITLE

COMMENT

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AL982948.1 GI:25186174 GSS. Danio rerio (zebrafish)

VERSION KEYWORDS SOURCE

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36.3%; Score 13.8; DB 9; Length 33; ilarity 72.0%; Pred. No. 9e+05; Conservative 0; Mismatches 7; Indels

Query Match Best Local Similarity Matches 18; Conserv

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A1223998
46 bp mRNA linear EST 21-DEC-1998
qx125107.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone lnAGE:2001181 3'
similar to TR:004154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15
PRECURSOR. ;contains element MER22 repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 07-JUN-2001
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
/clone lib="NCI_CGAP_Lym12"
/note="Togan: lymph node; Vector: pCMV-SPORT6; Site 1:
Sal; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Buarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 46)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tanional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Thuor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="lymphoma, follicular mixed small and large"
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ED75bl0.x1 Zebrafish WashU MPIMG EST Danio rerio CDNA clone
IMAGE.3717691 3' similar to SW:CA19 HUMAN P20849 COLLAGEN ALPHA
1(IX) CHAIN PRECURSOR.;, mRNA sequence.
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88.2%; Pred. No. 9.4e+05;
iive 0; Mismatches 2;
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Pred. No. 9.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 1534 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2001181"
                                                                                                                                                                                                              15 GGGGACTTTCCAGGGGG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI223998.1 GI:3806711
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AI544460/c
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AI223998/c
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

[Cypriniformes; Cyprinidae; Danio.

[Cypriniformes; Cyprinidae; Danio.

[Cypriniformes; Cyprinidae; Danio.

[Compara, S.J., Huckle, E. and Hunt, S.E.

[Compara, Sidential (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: Hunguery@anger.ac.uk Unpublished

[This sequence was generated from the SP6 end of BAC 4802. 48012 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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43 bp mRNA linear EST 13-APR-1999 ti06c03.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2129668 3' similar to TR:000599 000599 CON1. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Mammalia, Homo.

1 (Dases 1 to 43)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                      Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.8; DB 11;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                          1. .41
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DNEY-4812"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trace considered overall poor quality
Insert Length: 1286 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2129668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CGCTGGGGACTTTCCAGGGGGACTT 35
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Homo sapiens
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Unpublished (1997)
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Best Local Similarity
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ORGANISM
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TITLE
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KEYWORDS
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Man was in

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BJ057570 HBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL104h07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Kenopodinae, Kenopus, Kenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
                                                                                                                                                                                                                                                                                                                                                                     1 (Dases 1 to 46)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.3%; Score 13.8; DB 3; Length 46; 66.7%; Pred. No. 9.5e+05; Live 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Conteat: Tadams Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                 Kenopus laevis (African clawed frog)
Kenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed genes in X. laevis embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL104h07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp
The information of this clone
URL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111 Yata, Mishima,
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
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AUTHORS
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                                                 RESULT 42
BJ057570
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 46)

Stark, Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Mattin, J., Beck, C., Wylie, T.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

Washu Zebrafishe EST Project 1998

L. Ontact: Stephen L. Johnson

Washington University School of Medicine

Washington University School of Medicine

4444 Forcest Park Parkway. Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."
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Possible reversed clone: similarity on wrong strand
Seg primer: T7 ET from Amersham
High quality sequence stop: 1
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Pred. No. 9.5e+05;
0; Mismatches 12
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/organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:7955"
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                            EST.
Danio rerio (zebrafish)
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  AI544460.1 GI:4461833
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Best Local S:
Matches 21
                                                                              ORGANISM
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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is available through the following

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AU102496 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP22967, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases', rc.50)
Suruki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
12 GCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                14 GCTGGGAAGTTGACAGGGNGTTTANCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO Rep. 2 (5), 388-393 (2001)
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Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
PUBMED
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BH812215 32 bp DNA linear GSS 02-MAY-2002 SALK 061414 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_061414, genomic survey sequence.
                                                              CRI78464 S0 bp DNA linear GSS 06-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP340e12, genomic survey sequence. CRI78464
                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Ebarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Eogers, J. and Bradley, A.

Direct Submission
Submitted (20-FRB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeeke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis Genome Unpublished (2001)
Unpublished (2001)
Contact Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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88.2%; Pred. No. 9.6e+05;
ative 0; Mismatches 2;
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                                                                                                                                                                  CR178464.1 GI:49957313
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .50
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP340e12"
/clone_lib="MHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="genomic DNA"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 GCTGGCGACATTCCAGG 22
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KEYWORDS
SOURCE
ORGANISM
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                                   RESULT 45
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tckyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 bp mRNA linear EST 28-JAN-2004 AUIO7397 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone LNG13032, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 50)
Sauxuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Sakaki, Y., Maramura, Y., Suyama, A. and Sugano, J., Sese, J., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/mol_tracen:9606"
/clone="HEP22967"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_cref="taxon:9606"
/clone="LWG13032"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                    Length 50;
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36.3%; Score 13.8; DB 1;
Best Local Similarity 63.6%; Pred. No. 9.6e+05;
Matches 21; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.8; DB 1;
Pred. No. 9.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTTTCCGCTCGGCTGTTTCCTGCGCAGGTTTC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 GGAGACAATTCCTTGCTGACTGTCCAGGCAGTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    ch 36.3%;
l Similarity 63.6%;
21; Conservative
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Best Local Similarity
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nhimsanger ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU327/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 13-DEC-2000
                                                                                                                                                                                                                                                    chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (Dasses it. 0 41)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Direct Submission
Project, Sanger Centre, The Wellcome Trust Genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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ilarity 67.9%; Pred. No. 1.1e+06;
Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                            Query Match
35.8%; Score 13.6; DB 9;
Best Local Similarity 67.9%; Pred. No. 1.1e+06;
Matches 19; Conservative 0; Mismatches 9;
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/strain="TREU927"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL452967.1 GI:11850952
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Best Local Similarity
Matches 19; Conserv
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                       /db xref="txxon:3702"
/clone="SALK 061414"
/clone="SALK 061414"
/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 16-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Murcidea, Muridae, Murinae, Mus.

1 (bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ775335
2M0007G07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0007G07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb plasmid UDCCM library"
/note="Vector: PWB4Zhry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                     35.8%; Score 13.6; DB 9; Length 32; 80.0%; Pred. No. 1.1e+06;
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Fax: 801 585 7177
Bmail: ddunmgenetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0007 row: G column: 07
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0007G07"
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Mus musculus
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84112, USA
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E. 1 (bases 1 to 45)

B. Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schallenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Walerston, R., Wylie, T., Lennon, G., Soares, B., Wilson, R. and The WashU-HMI Mouse EST Project

I. Unpublished (1996)

Contact: Marra M/Mouse EST Project
Washington University School of Medicinep

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 bp mRNA linear EST 01-OCT-1997 ma41b12.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:313247 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLML ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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High quality sequence stop: 1.
Location/Qualifiers
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AI635210.1 GI:4686540
EST.
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AI635210/c
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VERSION
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W10989/c
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Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Arrayed by: Greg Lennologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NG.-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
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/lab_host="DH108"
/clone lib="NCI_CGAP_Ut2"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #:
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Homoinidae; Homo.

1 (bases 1 to 46)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Insert Length: 1695 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence scop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity 61.1
Matches 22; Conservative
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